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**BEFORE THE BOARD OF PATENT APPEALS
AND INTERFERENCES**

Application Number: 10/699,024
Filing Date: October 31, 2003
Appellant(s): ABDEEN HUSSAN, JAGIR RAZAK JAINUL

ANTHONY V.S. ENGLAND
For Appellant

EXAMINER'S ANSWER

This is in response to the appeal brief filed 03/07/2011 appealing from the Office action mailed 10/07/2010.

(1) Real Party in Interest

A statement identifying by name the real party in interest is contained in the brief.

(2) Related Appeals and Interferences

The examiner is not aware of any related appeals, interferences, or judicial proceedings which will directly affect or be directly affected by or have a bearing on the Board's decision in the pending appeal.

(3) Status of Claims

The statement of the status of claims contained in the brief is correct.

(4) Status of Amendments After Final

The appellant's statement of the status of amendments after final rejection contained in the brief is correct.

(5) Summary of Claimed Subject Matter

The summary of claimed subject matter contained in the brief is correct.

(6) Grounds of Rejection to be Reviewed on Appeal

The appellant's statement of the grounds of rejection to be reviewed on appeal is substantially correct.

(7) Claims Appendix

The copy of the appealed claims contained in the Appendix to the brief is correct.

(8) Evidence Relied Upon

The following is a listing of the evidence (e.g., patents, publications, Official Notice, and admitted prior art) relied upon in the rejection of claims under appeal.

Rigoutsos et al. (Bioinformatics, 1998, Vol. 14, No. 1, p. 55-67)

Chen et al. (Bioinformatics, 2002, Vol. 18, No. 12, p.1696-1698)

Orcutt et al. (Nucleic Acids Research, 1982, Vol. 10, No. 1, p. 157-174)

Zhang et al. (Genome Research, 1997, Vol. 7, p.649-656)

Martinez et al. (Nucleic Acids Research, 1983, Vol. 11, No. 13, p. 4629-4634)

UK CROPNETT (http://ukcrop.net/agr/sequence_display_key#sequence; Published 2001, p.1-5).

(9) Grounds of Rejection

The following ground(s) of rejection are applicable to the appealed claims:

Claim rejections - 35 USC § 112, 2nd Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 3-6, 10, 14-22 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claims that depend directly or indirectly from claim 14 are also rejected due to said dependence.

Claims 14, 24, 27, and 28 (see step viii) recites a step for generating a first instance of a sequence "wherein generating of the sequence is responsive to...", "...and responsive to the ...stored match-data entries", and "...the updating being responsive to the position." In each case, the recitation of the limitation "responsive" renders the claims indefinite for the following reasons. It is unclear in what way the computer generated sequence is "responsive to" backbone sequence data and stored match-set data. What positive limitation of the claimed system is intended by the phrase "responsive to"? For example, are these different types of data actually INPUT into the sequences? Similarly, it is unclear in what way a step of updating is "being responsive" to positional information. What positive limitation of the claimed **apparatus** is intended by the term "being responsive"? Applicant's amendments have not clarified this issue and the specification provides no guidance. For purposes of examination, the term

"responsive" is interpreted to mean "includes"; e.g. generating of the sequence includes the stored backbone sequence.

Claims 14, 24, 27, and 28 (see step x) recites the limitation "generating...a second instance of the sequence to a user responsive to the at least second one of the replets." In each case, the recitation of the limitation "responsive" renders the claims indefinite for the same reasons as those set forth above. As discussed above, it is unclear in what way a computer system generates a representation of a sequence to a user "responsive to" a stored backbone sequence and stored match-set data. What positive limitation of the claimed system is intended by the term "responsive to"? Applicant's amendments have not clarified this issue and the specification provides no guidance. For purposes of examination, the term "responsive" is interpreted as meaning "including."

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is

advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

The factual inquiries set forth in *Graham v. John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

Claims 4, 5, 14-22, 24, 27, and 28 are rejected under 35 U.S.C. 103(a) as being unpatentable over Rigoutsos et al. (Bioinformatics, 1998, Vol. 14, No. 1, p. 55-67), in view of Chen et al. (Bioinformatics, 2002, Vol. 18, No. 12, p.1696-1698), in view of Orcutt et al. (Nucleic Acids Research, 1982, Vol. 10, No. 1, p. 157-174), in view of Zhang et al. (Genome Research, 1997, Vol. 7, p.649-656), and in view of UK CROPNETT (http://ukcrop.net/agr/sequence_display_key#sequence; Published 2001, p.1-5).

CLAIM SUMMARY

The amended claims are now drawn to a computer system-implemented method for storing and presenting sequence data. Critical limitations of claims 1, 24, and 27 include specifying a set of replets for analysis by a computer system; ii) for each replet in the set, comparing each replet by the computer system to a sequence for determining

by the computer system a subsequence of the sequence that matches each replet, if any, wherein the sequence represents a genome sequence; iii) generating by the computer system responsive to the comparing, respective entries of a match-set data structure, the match-set data structure having respective entries for the each-respective reptiles, each entry comprising a sequence identification to identify a subsequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a first and second position parameter, iv) storing the generated entries of the match-set data structures in a computer readable memory by the computer system; v) deleting by the computer system each matching subsequence from the sequence where it is found; vi) concatenating by the computer system, in order, unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence; vii) the computer system generating or receiving a selection of at least a first one of the reptiles, wherein at least a portion of one of the matching subsequences is matched by a certain plurality of the reptiles and the received selection includes a selection of at least one of the certain plurality of reptiles; viii) the computer system generating a first instance of the sequence and presenting the first instance of the sequence to a user of the computer system, wherein the generating of the sequence is responsive to the stored backbone sequence and responsive to the at least one of the stored match-set data entries corresponding to the selected at least first one of the reptiles, wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second

position parameter of each match-set data structure entry denotes an offset from the location, wherein the selected at least first one of the replets has a position within the sequence, and wherein after receiving the selection the computer system updates the first and second parameters of the entries in the match-set data structure the updating being responsive to the position of the selected at least first one of the replets; ix) the computer system generating or receiving a selection of a second one of the replets and x) the computer system generating or receiving a selection of a second one of the replets and x) the computer system generating and presenting a second instance of the sequence to a user responsive to at least second one of the replets and wherein the computer system performs the generating of the second instance of the sequence by reference to the updated first and second parameters for the second one of the replets. For purposes of examination, the term replets is interpreted as patterns used to represent sequences, in light of the specification [p.7].

PRIOR ART

Rigoutsos teaches a computer-based program (i.e. TEIRESIAS) for discovering biological sequences [Abstract and p.56]. In particular, the program generates pattern entries representing a sequence [See Table 2], which meets claim language for specifying a set of replets in view of applicant's Remarks filed 11/04/2009 [page 7]. The program compares smaller sequences to a larger sequence and generates matching subsequences [p.56, col. 2, ¶3-bottom, and Fig. 1], which meets the claim language for generating entries of match-set data having respective entries for replets. This process includes identifying sequence ID and offset information for each matching subsequence

[p.56, col. 2, ¶3-bottom, and Fig. 1], which is a teaching for sequence identification to identify a sequence where a match occurs and offset information to determine position. New patterns are constructed based on previous sequences and parameters via an iterative convolution method [p.58, Col. 1, Fig. 3, p.59, Col. 1], which shows generating updated instances of sequence by reference to previous parameters. New offset lists are generated [p.58, Col. 1]. The program obtains optimal patterns and performs pattern-based searches of databases, and displays discovered pattern results in the form of sequences [p.56, Col. 1, and p.66, Col. 1 and Fig. 4, Table 2 and 4], which shows storing generated entries. Search results are tracked according to exact matches, matches within varying degrees of accuracy, and unmatched data [Table 5].

Rigoutsos does not specifically teach offset information having a first position parameter and a second position parameter, as in claims as in claims 14, 27, and 28 (step v). However, Rigoutsos provides a notation (indicated as LsP) that uses a sequence ID parameter (i) and an offset position parameter (j) denoting sequence matches at a specific offset; see p.56, Col. 2, ¶3 to bottom, and Figure 1, which suggests the use of first and second position parameters, because the sequence IDs taught by Rigoutsos are associated with positions (in a sequence) and the offset parameter taught by Rigoutsos denotes the offset position of the matching sequence. Therefore, Rigoutsos makes obvious the use of an offset information having a first position parameter and a second position parameter.

Rigoutsos does not teach deleting each matching subsequence from the sequence where it is found, as in claims 14, 27, and 28 (step v).

Rigoutsos does not teach concatenating unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence, as in claims 14, 24, and 27 (step vi).

Rigoutsos does not teach generating a presenting sequences that include stored backbone sequence and at least one of the stored match-set data entries corresponding to the selected at least first one of the replets, as in claims 14, 24, and 27 (step viii).

Rigoutsos does not teach updating the first and second parameters of the entries in the match-set data structure to include the position of the selected at least first one of the replets, as in claims 14, 24, and 27 (step viii).

Rigoutsos does not teach generating or receiving a selection of a second one of the replets and x) the computer system generating and presenting a second instance of the sequence to a user responsive to at least second one of the replets and wherein the computer system performs the generating of the second instance of the sequence by reference to the updated first and second parameters for the second one of the replets, as in claims 14, 24, and 27 (steps ix and x).

Chen teaches a program for identifying repeats in long DNA sequences [Introduction]. In particular, the program performs a step for extracting repeats and concatenates regions (other than repeats) and sends the string as input to another program [p.1697, Col. 2, p.1698, Col. 1, and Fig. 1]. The program also performs encoding of repeat regions in the DNA sequences [p.1696-97, Methods]. A graphic interface is provided for searching a sequence database using user-defined parameters

[Fig. 6]. This program is beneficial for improving search results through sequence compression [Introduction].

Orcutt teaches a nucleic acid sequence database computer system and program [Fig. 1]. The user can extract and concatenate any of the stored sequences, the complement, or the protein translations [p.168]. Sequences can be stored and examined by other matching programs [p.168]. Orcutt teaches updating the information stored in the computer system by considering old data, adding new data, and deleting old data, where the data can include files codes, indexes, sequence information, etc. [p.168], which teaches a computer system capable of updating parameters after receiving a selection. Orcutt also teaches updating a sequence database containing match-set data [p.169]. The system contains print functions for displaying the contents of any file [p.165]. The system provides match functions for determining sequence matches and mismatches program, and outputs a representation of a sequence in response to a matching program that considers contiguous residues that match [p.164, last ¶, p.167]. The system will also search and identify non-exact matches [p.165], which meets claim language for non-selected reptiles.

UK CROPNET teaches a computer based method for graphically displaying sequences from a database. In particular, the generated displays include a combination of different sequence information including BLAST matches to an insert sequence, homology matches to an insert sequence, introns, exons, textual information [See pages 2-3]. Additionally, graphs are generated to include representations of physical

positions of a probe in a region of a chromosome, backbone markers, and specific sequence information [p.4].

Zhang teaches a computer-based method for identifying and graphically displaying repeat regions on a gene [Abstract, Fig. 1]. The program also displays gaps, mismatches (i.e. non-matching) regions, gaps, and multiple alignments [Fig. 2, Fig. 3]. The program interface also allows for searching a database and using filtering commands [Fig. 6], which inherently functions to remove data from a viewable data set (i.e. deletion). The program is beneficial for creating user friendly interpretation for viewing results when matching database sequences [Abstract].

Regarding claim(s) claims 14, 27, and 28 (step v), it would have been obvious to someone of ordinary skill in the art at the time of the instant invention to have deleted each matching subsequence from the sequence where it is found, in the method of Rigoutsos, with a reasonable expectation of success, since Chen and Orcutt teach programs for deleting repeats and concatenating any stored sequences, as set forth above. The motivation would have been to improve searching by reducing the amount of data for processing, as suggested by Orcutt [p.157], or through sequence compression, as shown by Chen [Introduction].

Regarding claim(s) claims 14, 27, and 28 (step vi), it would further have been obvious to have concatenated unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence, in the method made obvious by Rigoutsos, Chen, and Orcutt, with a reasonable expectation of success, since Orcutt provides software for displaying and updating unmatched data

sets, as shown above, and since Zhang teaches a program for identifying and graphically displaying repeat mismatches (i.e. non-matching) regions, and multiple alignments, as set forth above. The motivation would have been to improve sequence analysis using a user friendly program for viewing results when matching database sequences, as set forth above Zhang.

Regarding claim(s) claims 14, 27, and 28 (step viii), it would have been obvious to someone of ordinary skill in the art at the time of the instant invention to have generated sequences including backbone sequences and at least one of the stored match-set data entries corresponding to the selected at least first one of the replets, in the method made obvious by Rigoutsos, Orcutt, and Chen, with a reasonable expectation of success, since the match sequences taught by Rigoutsos are generated by a computer using a reference sequence; p.58, col. 2, and Fig. 1, which suggests sequences generated in response to a backbone sequence, since Rigoutsos teaches reconstructing new patterns using stored match patterns; p.57, col. 2, and Fig. 2, which suggests the use of stored match set data, and in view of UK CROPNET, which teaches displaying sequences using a program that includes stored match-set data [See pages 2-3], as well as positional data and backbone sequences [p.4]. The motivation would have been to improve sequence analysis using a user friendly program for viewing results when matching database sequences, as suggested by Zhang.

Regarding claim(s) claims 14, 27, and 28 (step viii), it would have been obvious to someone of ordinary skill in the art at the time of the instant invention to have updated the first and second parameters of the entries in the match-set data structure to

include the position of the selected replets, in the method made obvious by Rigoutsos, Orcutt, and Chen, since ANY new computer generated match sequences taught by Rigoutsos are associated with a sequence ID parameter and an offset parameter, which suggest sequences with "updated" position and offset parameters. Furthermore, one of ordinary skill in the art would have recognized computational methods for updating parameters, such as by generating new patterns based on positional and offset information, as shown by Rigoutsos; page 58, col. 1 and Fig. 3, which suggests "updating" match-set data based on the position of selected replets. The motivation would have been to generate all matching patterns and quickly discard non-optimal patterns, as suggested by Rigoutsos; p. 58, col. 2.

Regarding claim(s) claims 14, 27, and 28 (steps ix and x), it would have been obvious to someone of ordinary skill in the art at the time of the instant invention to have generated a second instance of a sequence by reference to the updated first and second parameters for the second one of the replets, in the method made obvious by Rigoutsos, Chen, Orcutt, and Zhang, with a reasonable expectation of success, since Rigoutsos provides an iterative method for obtaining optimal replets and generating a plurality of sequence matches, as set forth above, and since Zhang shows that new sequences can be generated by filtering a database using user-defined parameters with predictable results, as set forth above, which suggests generating new sequences by reference to updated first and second parameters. The motivation would have been to improve sequence analysis using a user friendly program for viewing results when matching database sequences, as set forth above Zhang.

Claims 3-6, 10, 14-22, 24-28 are rejected under 35 U.S.C. 103(a) as being unpatentable over Rigoutsos et al. (Bioinformatics, 1998, Vol. 14, No. 1, p. 55-67), in view of Chen et al. (Bioinformatics, 2002, Vol. 18, No. 12, p.1696-1698), in view of Orcutt et al. (Nucleic Acids Research, 1982, Vol. 10, No. 1, p. 157-174), in view of Zhang et al. (Genome Research, 1997, Vol. 7, p.649-656), in view of UK CROPNETT (Published 2001, p.1-5), and in view of Martinez et al. (Nucleic Acids Research, 1983, Vol. 11, No. 13, p. 4629-4634).

Rigoutsos, Chen, Orcutt, Zhang, and UK CROPNET make obvious the method, system, and computer readable medium of claims 4, 5, 14-22, 24, 27, and 28, as set forth above.

Rigoutsos, Chen, Orcutt, Zhang, and UK CROPNET do not specifically teach storing multiple views of the sequence data at multiple levels of abstraction, as in claim 10. However, this limitation would have been obvious to one of ordinary skill in the art at the time of the invention since both Zhang and UK CROPNET teach computer programs that are capable of graphically displaying sequence data comprising various types of data, and since UK CROPNET teaches the use of different known graphical schemes for distinguishing data, such as viewing the data using different colors, as set forth above, which reasonably suggests the claimed limitation. The motivation would have been to improve sequence analysis using a user friendly program for viewing results when matching database sequences, as taught by Zhang, above.

Rigoutsos, Chen, Orcutt, Zhang, and UK CROPNET do not teach storing information in a table using a "pointer", as in claims 3, 6, and 25.

Martinez teaches a computer program for finding repeats in molecular sequences using pointers to indicate order and variation between sequences [Abstract and p.4630].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to have stored information in a table using a pointer, in the method, system, and computer readable media made obvious by Rigoutsos, Chen, Orcutt, Zhang, and UK CROPNET, with a reasonable expectation of success, since Martinez teaches a program that finds repeats in molecular sequences using pointers, as shown above. The motivation would have been to indicate order and variation between sequences, as shown by Martinez [p.4630, 4634].

(10) Response to Argument

Rejection of claims 3-6, 10, 14-22 under 35 U.S.C. 112, second paragraph

Appellant's arguments have been fully considered but are not persuasive for the following reasons. In response to appellant's arguments, on page 16, that the limitation "responsive to" (claim 14, step viii) is not indefinite because it is analogous to a mathematical function that "x is a function of u and v", mathematical functions have well defined equations, parameters, and most importantly allow for INPUT and OUTPUT. The sequences as claimed have none of these features, and therefore are not equivalent mathematical equations. Furthermore, even if the claimed sequences were equivalent to a mathematical function, appellant has not clarified in what way the

generated sequence is "responsive to" backbone sequence information and stored match-set data entries. For example, are these different types of data actually INPUT into the sequences? If so, what is the OUTPUT? The specification provides no such guidance. Therefore the examiner maintains that it is unclear what positive limitation of the system, if any, is intended by the term "responsive to", such that one of ordinary skill in the art would understand the metes and bounds of the generated sequence.

Appellant's response has not addressed the limitation "the updating being responsive to the position of selected replets" (claim 14, step viii). However, this limitation remains unclear because appellant has not clarified what functional limitation of the claimed system, if any, is intended by the term "being responsive". What positive limitation of the claimed system is intended by updating "being responsive" to the position of replets? The specification does not provide any guidance. Therefore, one of ordinary skill in the art would not understand the metes and bounds of the "updated" first and second parameters.

Appellant's response has not addressed the limitation "generating...a second instance of the sequence to a user responsive to the at least second one of the replets" (claim 14, step x). However, the recitation of the limitation "responsive" renders the claims indefinite for the same reasoning as discussed above. Namely, it remains unclear in what way a computer system generates a representation of a sequence to a user "responsive to" a stored backbone sequence and stored match-set data such that one of ordinary skill in the art would understand the metes and bounds of the

representation that is generated for said user. Applicant's amendments have not clarified this issue and the specification provides no guidance.

Rejection under 35 U.S.C. 103(a) over Rigoutsos et al. in view of Chen et al., Orcutt et al., and in view of UK CROPNETT

Appellant's arguments have been fully considered but are not persuasive for the following reasons. In response to appellant's argument, on page 17, that the office actions have been unclear with regards to the teachings of the prior art reference, the Examiner has clearly cited the teachings of each cited reference and pointed to specific locations of these teachings within the references in each of the Office actions. The Examiner has also given the claims their broadest reasonable interpretation and applied appropriate prior art despite the issues of indefiniteness (as discussed above).

In response to appellant's aggregate arguments, on pages 18-19, that the prior art of Rigoutsos only teaches a single parameter for offset information and fails to teach offset information comprising first and second position parameters, it was acknowledged that Rigoutsos does not specifically teach offset information having a first position parameter and a second position parameter, as set forth above. However, Rigoutsos provides a notation (indicated as LsP) that allows for the COMBINED representation of a sequence ID parameter (i) and an offset position parameter (j) denoting sequence matches at a specific offset, collectively represented as (i,j); see p.56, Col. 2, ¶3 to bottom, and Figure 1, which suggests the use of first and second position parameters, because the sequence IDs taught by Rigoutsos are associated with positions (in a

sequence) and the offset parameter taught by Rigoutsos represents the offset position of the matching sequence. Therefore, Rigoutsos makes obvious the use of offset information having a first position parameter and a second position parameter.

In response to appellant's arguments, on page 19, that Rigoutsos does not teach identifying match-set entries having both a sequence identification to identifying where a match occurs and offset information to determine a position within the sequence where the matching subsequence is located, Rigoutsos provides a method for identifying where the matching subsequences occur within a larger sequence, provides what sequences are matching, and provides the offset positions of these subsequence within the larger sequence [p.56, col. 2, ¶13-bottom], as explained above.

In response to appellant's aggregate arguments, on pages 20-22, that Rigoutsos does not teach updating first and second parameters of match-set data, it would have been obvious to one of ordinary skill in the art to have "updated" the first and second parameters associated with the match-data sets (made obvious by Rigoutsos), since ANY computer generated match sequence taught by Rigoutsos is associated with a sequence ID parameter and an offset parameter. Therefore newly generated match sequences are "updated" with new position and offset parameters. Furthermore, one of ordinary skill in the art would have recognized computational methods for updating parameters, such as by generating new patterns based on positional and offset information, as shown by Rigoutsos; page 58, col. 1 and Fig. 3, which suggests "updating" match-set data based on the position of selected replets. The motivation would have been to generate all matching patterns and quickly discard non-optimal

patterns, as suggested by Rigoutsos; p. 58, col. 2. It is additionally noted that the neither applicant's arguments, the claims, nor the specification provides any illuminating guidance as to what is required for updating parameters, wherein the updating is "being responsive to the position of selected" replets (i.e. sequences), as recited in the claims.

In response to appellant's arguments, on pages 21, regarding *KSR International Co. v. Teleflex Inc.*, 550 U.S. 398 (2007), the rejection of step viii) has been modified after a further review of the teachings of Rigoutsos, who provides all the necessary teachings (and suggestions) to make a case for prima facie obviousness with regards to the step of "updating" first and second parameters of match-set data, as set forth above. Accordingly, appellant's arguments on this point are moot. It is noted that KSR was correctly applied because the prior art of Rigoutsos either teaches or suggests the updating of first and second parameters, and reasons for combining the various references were set forth above.

In response to appellant's arguments, on page 23, that the combination of Rigoutsos, Chen, Orcutt, and UK CROPNETT does not teach "viii) the computer system generating a first instance of the sequence and presenting the first instance to a user of the computer system, wherein the sequence is responsive to the stored backbone sequence and the stored match set data entries", Rigoutsos teaches computer generated match sequences using a reference sequence; p.58, col. 2, and Fig. 1, which suggests sequences generated in response to a backbone sequence. Rigoutsos teaches reconstructing new patterns using stored match patterns; p.57, col. 2, and Fig. 2, which suggests the use of stored match set data. Furthermore, one of ordinary skill in

the art would have recognized methods for displaying ANY combination of information including matches to an insert sequence, sequence position, as well as positional data and backbone sequences, in view of UK CROPNET [See pages 2-4]. As set forth above, the motivation to combine these references would have been to improve sequence analysis using a user friendly program for viewing results when matching database sequences, as suggested by Zhang.

Therefore, all the elements of Applicant's invention with respect to the specified claims are instantly disclosed or fully envisioned by the combination of references cited above.

Rejection under 35 U.S.C. 103(a) over Rigoutsos et al. in view of Chen et al., Orcutt et al., in view of UK CROPNETT, and in view of Martinez et al.

Appellant's arguments have not set forth any additional or specific arguments regarding the teachings of Martinez. Therefore, the examiner maintains that the combination of Rigoutsos et al. in view of Chen et al., Orcutt et al., in view of UK CROPNETT, and in view of Martinez et al. teaches and/or makes obvious the claimed limitations for the reasons set forth above.

(11) Related Proceeding(s) Appendix

No decision rendered by a court or the Board is identified by the examiner in the Related Appeals and Interferences section of this examiner's answer.

For the above reasons, it is believed that the rejections should be sustained.

Respectfully submitted,

/Pablo S. Whaley/

Patent Examiner, AU 1631

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